REFERENCE TITTE JOURNA: TURES REFERENC COMMENT Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Mgene, C., Zvans, C.A., Falls, T., Fan, G., Fringy, M., Fladgy, M., Gotter, M., Foster, M., Franca, F., Fringy, M., Fladgy, M., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Kall, R., Grady, M., Guerra, M., Gunarathe, P., Haaland, W., Manil, C., Hamilton, C., Hamilton, K., Mallins, B., Howells, S., Hilly, M., Johnson, B., Johnson, R., Jolivet, A., Josephy, S., Kelly, S., Khah, K., Khang, L., Kovar, C., Kowis, C., Krafft, K., Lebow, H., Lowan, M., Lewis, L., Liu, J., Liu, J., Liu, M., Liu, Y., London, P., Longacke, S., Lopez, J., Lorensubewa, T., London, P., Longacke, S., Lopez, J., Lorensubewa, T., London, P., Longacke, S., Lopez, J., Liu, J., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Martin, K., Martin, R., Martin, R., Martin, K., Martin, R., Martin, M., More, S., McLeod, M.P., Mortin, R., Martin, M., Morris, K., Mortin, M., Morris, M., Morris, K., Martin, M., Morris, M., Morris, M., Martin, M., Marti 2535 1759 2595 1819 JONN-2002 190301 bp DNA linear HTG 19-NOV-2002 Rattus norvegicus clone CH230-442A4, WORKING DRAFT SEQUENCE, 2 CCCGGGCGCGCAAGAAGAAACTCAGCAAGTCAGATATCATGTTGGTGCAGGGCGCGAACG 2475 2656 CCATCGTCACCGGGTACAGCGACCAGCAACCAGACATTTCCAACGGAAGCATTTGT 2715 TGTTCCTGAAGCCCTGCAGCCCTTCCCGGAGTACAGATGCTGAGCACAATCCCTGCGGAG 2655 Mukny, D. Marie., Merzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Alsbrooks, S., Amin, A., Anguianco, D., Angai, A., Ayodgi, A., Ayodgi, M., Baca, E., Baden, H., Bardwinto, Bandaranaike, D., Barber, M., Barnskead, M., Benamed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, F., Brown, M., Canderon, E., Cardenas, V., Carter, K., Cavacron, E., Cardenas, V., Carter, K., Cavacron, E., Chacko, J., Chwez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cen, G., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davye, C., Davy-Carroll, K., Duhah, K., Dudan, R., Dagar, R., Da ostomi; TGTTTCTTAAGCCCTGCAGCCCTTCGCGGAGTACGGACACTGAGCACAACCCCTGCGGGG TACCCAGTAACCCGGCCCAGGTGCCGATAGAGGAGTCCGGGGGGCTTTGGCTCCCACCACC CCATCGTCACCGGTTACACCGACCAGCCTGATATCATCTCCAACGGAAGCATTTTGT receraceascesses de de construcción de la contracea de con ACAACCAGAATTACTGCTATCAGGTATGCCTGACCCCTGAGTCCGCCAAGACCGGACCTGA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutey6osto Mammalia; Eutheria; Rodentía; Sciurognathi; Muridae; Myfinae; Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Par Pasternak,S., PaullH., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., P.L.L... Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., R DRAFT; HTGS_FULLTOP 1880 CCAACGAGACTAAACACCAGCGAGCAGGAGCTC 1911 CCAACGAGGTAAGGCTGAAGGAAAGAAGCAC 2747 HTG: HTGS PHASE1; HTGS DRAFT; F Rattus norvegicus (Norway rat) Rattus norvegicus AC119377.4 GI:25095811 (bases 1 to 190301) Rattus. 1640 1700 2596 1820 2416 1760 LOCUS CESSION KEYWORDS SOURCE AUTHORS REFERENCE AC119377 VERSION ORGAN qq ઠે q ò q ò g ò ò

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Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics Baylor College of Medicine, One Baylor Maza, Houston, TX 77010, USA and Medicine, One Baylor Maza, Houston, TX 77010, USA and Medicine, One Sequence in this sequence version replaced gi:22856365.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequence yearson of BAC based reads and hole genome shotgun sequence tall the Cally of Carl Contig described in the feature table below represents a scaffold in the Atlas assembly (a contig-scaffold). Within each contig-scaffold, individual sequence configs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the fends of the clone and there may be sequence
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(see http://www.hgsc.bcm.tmc.edu.docs/Gerbank_draft_data.html).

NOTE: This is a "working draft' sequence It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of Molecular and Human Genetics, Bayjor Coilege of Medicine, One Bytor Plaza, Houston, TX 77030, USA (bases 1 to 1002)
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                                                                                                                                                                                                                                                        Kaylor, C.,
Usmani, K.,
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Assembly program: Phrably version 0.990329
Consensus quality: 174669 bases at least Q40
Consensus quality: 176582 bases at least Q30
Consensus quality: 177866 bases at least Q30
Estimated insert size: 181269; sum-of-contigs estimation
Obality coverage: 7x in Q20 bases; sum-of-contigs estimation
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h, D., von
A., Smith, H.O.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F. Ries, C., Rodkey, C., Rojas, M., Rose, R., Rulis, S., Sanders, W., Savedkey, G., Scherer, S., Scott, G., Shatsman, S., Sherty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, S., Scott, G., A., Sodergren, E., Song, X., Z., Soreile, R., Sosa, J., Streamle, M., Strong, R., Sutton, A., Svatex, A., Tabox, P., Usman, Valas, R., Vera, V., Villasana, D., Waldon, L., Walter, F., Wang, C., Warg, S., Warten, R., Wocden, H., Wriey, K., Willson, R., Wieczyk, R., Wooden, H., Wriey, K., Wight, D., Wang, C., Warg, C., Wang, C., Warght, D., Wallson, R., Wieczyk, R., Wooden, H., Wriey, K., Wieczyk, R., Wooden, H., Wriey, K., Wang, C., Wang,
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188804 188903: gap of unknown length
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Location/Qualifiers
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Direct Submission
Submitted (26-APR-2002) Human Genome
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Contact: hgsc-help@bcm.tmc.edu
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